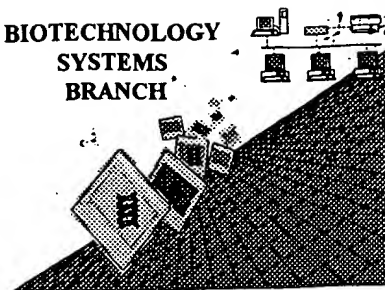


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/701,080
Source: PCT/09
Date Processed by STIC: 8/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,080

DATE: 08/01/2001

TIME: 19:28:28

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\08012001\I701080.raw

3 <110> APPLICANT: O'CONNOR, MARK J.
 4 ZIMMERMAN, HOLGER
 6 <120> TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN
 P300 FOR USE IN
 7 TRANSCRIPTIONAL REGULATION
 9 <130> FILE REFERENCE: 117-328
 11 <140> CURRENT APPLICATION NUMBER: US 09/701,080
 12 <141> CURRENT FILING DATE: 2001-02-27
 14 <150> PRIOR APPLICATION NUMBER: GB 9811303.8
 15 <151> PRIOR FILING DATE: 1998-05-26
 17 <150> PRIOR APPLICATION NUMBER: GB 9900157.0
 18 <151> PRIOR FILING DATE: 1999-01-05
 20 <160> NUMBER OF SEQ ID NOS: 36
 22 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

286 <210> SEQ ID NO: 20
 287 <211> LENGTH: 13 *13/2 shown (p.2)*
 288 <212> TYPE: PRT
 289 <213> ORGANISM: Artificial Sequence
 291 <220> FEATURE:
 292 <221> NAME/KEY: VARIANT
 293 <222> LOCATION: (1)
 294 <223> OTHER INFORMATION: Xaa represents Lys or Arg
 296 <220> FEATURE:
 297 <221> NAME/KEY: VARIANT
 298 <222> LOCATION: (2)
 299 <223> OTHER INFORMATION: Xaa represents Lys or Arg
 301 <220> FEATURE:
 302 <221> NAME/KEY: VARIANT
 303 <222> LOCATION: (3)
 304 <223> OTHER INFORMATION: Xaa represents any amino acid
 306 <220> FEATURE:
 307 <221> NAME/KEY: VARIANT
 308 <222> LOCATION: (5)
 309 <223> OTHER INFORMATION: Xaa represents any amino acid
 311 <220> FEATURE:
 312 <221> NAME/KEY: VARIANT
 313 <222> LOCATION: (6)
 314 <223> OTHER INFORMATION: Xaa represents any amino acid
 316 <220> FEATURE:
 317 <221> NAME/KEY: VARIANT
 318 <222> LOCATION: (9)
 319 <223> OTHER INFORMATION: Xaa is Val or Ile
 321 <220> FEATURE:
 322 <221> NAME/KEY: VARIANT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/701,080

DATE: 08/01/2001

TIME: 19:28:28

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\08012001\I701080.raw

323 <222> LOCATION: (11)
 324 <223> OTHER INFORMATION: Xaa represents Lys or Arg
 326 <220> FEATURE:
 327 <221> NAME/KEY: VARIANT
 328 <222> LOCATION: (12)
 329 <223> OTHER INFORMATION: Xaa represents any amino acid
 331 <220> FEATURE:
 332 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus sequence of
 transcriptional adaptor
 333 motif (TRAM)
 335 <400> SEQUENCE: 20
 W- 336 Xaa Xaa Xaa Asn Xaa Xaa Cys Pro Xaa Cys Xaa Xaa
 E--> 337 1 5 10

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/701,080

DATE: 08/01/2001

TIME: 19:28:29

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\08012001\I701080.raw

L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:337 M:252 E: No. of Seq. differs, <211>LENGTH:Input:13 Found:12 SEQ:20
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22